

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

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Application Serial Number: 10/580,906
Source: 1FWP
Date Processed by STIC: 6/8/06

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

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1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
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Revised 01/10/06



IFWP

RAW SEQUENCE LISTING

DATE: 06/08/2006

PATENT APPLICATION: US/10/580,906

TIME: 10:08:05

Input Set : A:\Sequence Listing for RECEPTOR FUNCTION REGULATING

AGENT.txt

Output Set: N:\CRF4\06082006\J580906.raw

3 <110> APPLICANT: FUKATSU et al.
 5 <120> TITLE OF INVENTION: RECEPTOR FUNCTION REGULATING AGENT
 7 <130> FILE REFERENCE: 20039.0005USWO
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/580,906
 10 <141> CURRENT FILING DATE: 2006-05-26
 12 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/017996
 13 <151> PRIOR FILING DATE: 2004-11-26
 15 <150> PRIOR APPLICATION NUMBER: JP 2003-394848
 16 <151> PRIOR FILING DATE: 2003-11-26
 18 <160> NUMBER OF SEQ ID NOS: 20
 20 <170> SOFTWARE: PatentIn Version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 361
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Human
 W--> 26 <400> SEQUENCE: 1

28	Met	Ser	Pro	Glu	Cys	Ala	Arg	Ala	Ala	Gly	Asp	Ala	Pro	Leu	Arg	Ser
29					5					10					15	
30	Leu	Glu	Gln	Ala	Asn	Arg	Thr	Arg	Phe	Pro	Phe	Phe	Ser	Asp	Val	Lys
31				20					25					30		
32	Gly	Asp	His	Arg	Leu	Val	Leu	Ala	Ala	Val	Glu	Thr	Thr	Val	Leu	Val
33			35				40					45				
34	Leu	Ile	Phe	Ala	Val	Ser	Leu	Leu	Gly	Asn	Val	Cys	Ala	Leu	Val	Leu
35		50					55				60					
36	Val	Ala	Arg	Arg	Arg	Arg	Arg	Gly	Ala	Thr	Ala	Cys	Leu	Val	Leu	Asn
37	65				70					75					80	
38	Leu	Phe	Cys	Ala	Asp	Leu	Leu	Phe	Ile	Ser	Ala	Ile	Pro	Leu	Val	Leu
39				85					90					95		
40	Ala	Val	Arg	Trp	Thr	Glu	Ala	Trp	Leu	Leu	Gly	Pro	Val	Ala	Cys	His
41				100					105					110		
42	Leu	Leu	Phe	Tyr	Val	Met	Thr	Leu	Ser	Gly	Ser	Val	Thr	Ile	Leu	Thr
43			115					120					125			
44	Leu	Ala	Ala	Val	Ser	Leu	Glu	Arg	Met	Val	Cys	Ile	Val	His	Leu	Gln
45		130					135				140					
46	Arg	Gly	Val	Arg	Gly	Pro	Gly	Arg	Arg	Ala	Arg	Ala	Val	Leu	Leu	Ala
47	145					150				155				160		
48	Leu	Ile	Trp	Gly	Tyr	Ser	Ala	Val	Ala	Ala	Leu	Pro	Leu	Cys	Val	Phe
49				165					170					175		
50	Phe	Arg	Val	Val	Pro	Gln	Arg	Leu	Pro	Gly	Ala	Asp	Gln	Glu	Ile	Ser
51			180					185					190			
52	Ile	Cys	Thr	Leu	Ile	Trp	Pro	Thr	Ile	Pro	Gly	Glu	Ile	Ser	Trp	Asp
53			195				200					205				
54	Val	Ser	Phe	Val	Thr	Leu	Asn	Phe	Leu	Val	Pro	Gly	Leu	Val	Ile	Val

pp 4, 6
 Does Not Comply
 Corrected Diskette Needed

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55      210      215      220
56 Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
57 225      230      235      240
58 Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
59      245      250      255
60 Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
61      260      265      270
62 Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
63      275      280      285
64 Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
65      290      295      300
66 Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
67 305      310      315      320
68 Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
69      325      330      335
70 Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys
71      340      345      350
72 Arg Asn Asp Leu Ser Ile Ile Ser Gly
73      355      360

```

74 <210> SEQ ID NO: 2

75 <211> LENGTH: 1083

76 <212> TYPE: DNA

77 <213> ORGANISM: Human

W--> 78 <400> SEQUENCE: 2

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79 atgtcccctg aatgcgcgcg ggcagcgggc gacgcgcctt tgcgcagcct ggagcaagcc 60
80 aaccgcaccc gctttccctt cttctccgac gtcaagggcg accaccggct ggtgctggcc 120
81 gcgggtggaga caaccgtgct ggtgctcatc tttgcagtgt cgctgctggg caacgtgtgc 180
82 gccctgggtgc tgggtggcgcg ccgacgacgc cgcgggcgca ctgcctgcct ggtactcaac 240
83 ctcttctgcg cggacctgct cttcatcagc gctatccctc tgggtgctggc cgtgcgctgg 300
84 actgaggcct ggctgctggg ccccgttgcc tgccacctgc tcttctacgt gatgacctg 360
85 agcggcagcg tcaccatcct cagcctggcc gcggtcagcc tggagcgcct ggtgtgcatc 420
86 gtgcacctgc agcgcggcgt gcggggctct gggcggcgcg cgcgggcagt gctgctggcg 480
87 ctcatctggg gctattcggc ggtcgccgct ctgcctctct gcgtcttctt ccgagtcgtc 540
88 ccgcaacggc tccccggcgc cgaccaggaa atttcgattt gcacactgat ttggcccacc 600
89 attcctggag agatctcgtg ggatgtctct tttgttactt tgaacttctt ggtgccagga 660
90 ctggtcattg tgatcagtta ctccaaaatt ttacagatca caaaggcatc aaggaagagg 720
91 ctcacggtaa gcctggccta ctcgagagc caccagatcc gcgtgtccca gcaggacttc 780
92 cggctcttcc gcacctctt cctcctcatg gtctccttct tcatcatgtg gagccccatc 840
93 atcatcacca tcctcctcat cctgatccag aacttcaagc aagacctggt catctggccg 900
94 tccctcttct tctgggtggg ggccttcaca tttgctaatt cagccctaaa ccccatcctc 960
95 tacaacatga cactgtgcag gaatgagtgg aagaaaattt tttgctgctt ctggttccca 1020
96 gaaaaggagg ccattttaac agacacatct gtcaaaagaa atgacttgct gattatttct 1080
97 ggc 1083

```

98 <210> SEQ ID NO: 3

99 <211> LENGTH: 361

100 <212> TYPE: PRT

101 <213> ORGANISM: Mouse

W--> 102 <400> SEQUENCE: 3

103 Met Ser Pro Glu Cys Ala Gln Thr Thr Gly Pro Gly Pro Ser His Thr

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```

104          5          10          15
105 Leu Asp Gln Val Asn Arg Thr His Phe Pro Phe Phe Ser Asp Val Lys
106          20          25          30
107 Gly Asp His Arg Leu Val Leu Ser Val Val Glu Thr Thr Val Leu Gly
108          35          40          45
109 Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
110          50          55          60
111 Val Ala Arg Arg Arg Arg Gly Ala Thr Ala Ser Leu Val Leu Asn
112 65          70          75          80
113 Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile Pro Leu Val Leu
114          85          90          95
115 Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Val Cys His
116          100          105          110
117 Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val Thr Ile Leu Thr
118          115          120          125
119 Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val Arg Leu Arg
120          130          135          140
121 Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala Leu Leu Ala
122 145          150          155          160
123 Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu Cys Ile Leu
124          165          170          175
125 Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln Glu Ile Pro
126          180          185          190
127 Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile Ser Trp Asp
128          195          200          205
129 Val Phe Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
130          210          215          220
131 Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
132 225          230          235          240
133 Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
134          245          250          255
135 Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
136          260          265          270
137 Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
138          275          280          285
139 Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
140          290          295          300
141 Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
142 305          310          315          320
143 Tyr Asn Met Ser Leu Phe Arg Asn Glu Trp Arg Lys Ile Phe Cys Cys
144          325          330          335
145 Phe Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Asp Thr Ser Val Arg
146          340          345          350
147 Arg Asn Asp Leu Ser Val Ile Ser Ser
148          355          360
149 <210> SEQ ID NO: 4
150 <211> LENGTH: 1083
151 <212> TYPE: DNA
152 <213> ORGANISM: Mouse

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Output Set: N:\CRF4\06082006\J580906.raw

W--> 153 <400> SEQUENCE: 4

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154 atgtcccctg agtgtgcaca gacgacgggc cctggcccct cgcacaccct ggaccaagtc 60
155 aatcgcaccc acttcccttt cttctcggat gtcaagggcg accaccggtt ggtgttgagc 120
156 gtcgtggaga ccaccgttct ggggctcatc tttgtcgtct cactgctggg caacgtgtgt 180
157 gctctagtgc tgggtggcgcg ccgtcggcgc cgtggggcga cagccagcct ggtgctcaac 240
158 ctcttctgcg cggatttgc tttcaccagc gccatccctc tagtgctcgt cgtgcgctgg 300
159 actgaggcct ggctgttggg gcccgctcgtc tgccacctgc tcttctacgt gatgacaatg 360
160 agcggcagcg tcacgatcct cacactggcc gcggtcagcc tggagcgcag ggtgtgcatc 420
161 gtgcgcctcc ggcgcggtt gagcgggccg gggcgggcga ctcaggcggc actgctggct 480
162 ttcatatggg gttactcggc gctcgccgcg ctgcccctct gcactctgtt ccgcgtggct 540
163 ccgcagcgcc ttcccggcgg ggaccaggaa attccgattt gcacattgga ttggcccaac 600
164 cgcataggag aaatctcatg ggatgtgttt tttgtgactt tgaacttcct ggtgccggga 660
165 ctggtcattg tgatcagtta ctccaaaatt ttacagatca cgaaagcatc gcggaagagg 720
166 cttacgctga gcttggcata ctctgagagc caccagatcc gagtgtccca acaagactac 780
167 cgactcttcc gcacgctctt cctgctcatg gtttccttct tcatcatgtg gagtcccatc 840
168 atcatcacca tctcctcat cttgatccaa aacttcgggc aggacctggt catctggcca 900
169 tcccttttct tctgggtggt ggcccttcacg tttgccaact ctgccctaaa ccccatactg 960
170 tacaacatgt cgctgttcag gaacgaatgg aggaagattt tttgctgctt cttttttcca 1020
171 gagaagggag ccattttttac agacacgtct gtcaggcgaa atgacttgtc tgttattttc 1080
172 agc 1083

```

173 <210> SEQ ID NO: 5

174 <211> LENGTH: 20

175 <212> TYPE: DNA

176 <213> ORGANISM: Artificial Sequence

W--> 177 <220> FEATURE:

W--> 178 <223> OTHER INFORMATION:

W--> 178 <400> SEQUENCE: 5

179 gctgtggcat gcttttaaac 20

180 <210> SEQ ID NO: 6

181 <211> LENGTH: 20

182 <212> TYPE: DNA

183 <213> ORGANISM: Artificial Sequence

W--> 184 <220> FEATURE:

W--> 185 <223> OTHER INFORMATION:

W--> 185 <400> SEQUENCE: 6

186 cgctgtggat gtctatttgc 20

187 <210> SEQ ID NO: 7

188 <211> LENGTH: 30

189 <212> TYPE: DNA

190 <213> ORGANISM: Artificial Sequence

W--> 191 <220> FEATURE:

W--> 192 <223> OTHER INFORMATION:

W--> 192 <400> SEQUENCE: 7

193 agttcatttc cagtaccctc catcagtggc 30

194 <210> SEQ ID NO: 8

195 <211> LENGTH: 361

196 <212> TYPE: PRT

197 <213> ORGANISM: Rat

W--> 198 <400> SEQUENCE: 8

see p. 6 for error exploration

this error appears in other sequences too

RAW SEQUENCE LISTING

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Input Set : A:\Sequence Listing for RECEPTOR FUNCTION REGULATING

AGENT.txt

Output Set: N:\CRF4\06082006\J580906.raw

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199 Met Ser Pro Glu Cys Ala Gln Thr Thr Gly Pro Gly Pro Ser Arg Thr
200           5           10           15
201 Pro Asp Gln Val Asn Arg Thr His Phe Pro Phe Phe Ser Asp Val Lys
202           20           25           30
203 Gly Asp His Arg Leu Val Leu Ser Val Leu Glu Thr Thr Val Leu Gly
204           35           40           45
205 Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
206           50           55           60
207 Val Val Arg Arg Arg Arg Gly Ala Thr Val Ser Leu Val Leu Asn
208 65           70           75           80
209 Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile Pro Leu Val Leu
210           85           90           95
211 Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Val Cys His
212           100          105          110
213 Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val Thr Ile Leu Thr
214           115          120          125
215 Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val Arg Leu Arg
216           130          135          140
217 Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala Leu Leu Ala
218 145           150          155          160
219 Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu Cys Ile Leu
220           165          170          175
221 Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln Glu Ile Pro
222           180          185          190
223 Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile Ser Trp Asp
224           195          200          205
225 Val Phe Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
226           210          215          220
227 Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
228 225           230          235          240
229 Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
230           245          250          255
231 Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
232           260          265          270
233 Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
234           275          280          285
235 Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
236           290          295          300
237 Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
238 305           310          315          320
239 Tyr Asn Met Ser Leu Phe Arg Ser Glu Trp Arg Lys Ile Phe Cys Cys
240           325          330          335
241 Phe Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Glu Thr Ser Ile Arg
242           340          345          350
243 Arg Asn Asp Leu Ser Val Ile Ser Thr
244           355          360
245 <210> SEQ ID NO: 9
246 <211> LENGTH: 1083
247 <212> TYPE: DNA

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/580,906

DATE: 06/08/2006
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Input Set : A:\Sequence Listing for RECEPTOR FUNCTION REGULATING

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Use of <220> Feature(NEW RULES): *error explanation*
Sequence(s) __ are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:5,6,7,10,11,12,13,14,15,16,17,18,19,20

VERIFICATION SUMMARY

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Input Set : A:\Sequence Listing for RECEPTOR FUNCTION REGULATING

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:26 M:283 W: Missing Blank Line separator, <400> field identifier
L:78 M:283 W: Missing Blank Line separator, <400> field identifier
L:102 M:283 W: Missing Blank Line separator, <400> field identifier
L:153 M:283 W: Missing Blank Line separator, <400> field identifier
L:177 M:283 W: Missing Blank Line separator, <220> field identifier
L:178 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:178 M:283 W: Missing Blank Line separator, <400> field identifier
L:178 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:178
L:184 M:283 W: Missing Blank Line separator, <220> field identifier
L:185 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:185 M:283 W: Missing Blank Line separator, <400> field identifier
L:185 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:185
L:191 M:283 W: Missing Blank Line separator, <220> field identifier
L:192 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>
ORGANISM:Artificial Sequence
L:192 M:283 W: Missing Blank Line separator, <400> field identifier
L:192 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:192
L:198 M:283 W: Missing Blank Line separator, <400> field identifier
L:249 M:283 W: Missing Blank Line separator, <400> field identifier
L:273 M:283 W: Missing Blank Line separator, <220> field identifier
L:274 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:274 M:283 W: Missing Blank Line separator, <400> field identifier
L:274 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:274
L:280 M:283 W: Missing Blank Line separator, <220> field identifier
L:281 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>
ORGANISM:Artificial Sequence
L:281 M:283 W: Missing Blank Line separator, <400> field identifier
L:281 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:281
L:287 M:283 W: Missing Blank Line separator, <220> field identifier
L:288 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>
ORGANISM:Artificial Sequence
L:288 M:283 W: Missing Blank Line separator, <400> field identifier
L:288 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:288
L:294 M:283 W: Missing Blank Line separator, <220> field identifier
L:295 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:13, <213>
ORGANISM:Artificial Sequence
L:295 M:283 W: Missing Blank Line separator, <400> field identifier
L:295 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:295
L:301 M:283 W: Missing Blank Line separator, <220> field identifier
L:302 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>
ORGANISM:Artificial Sequence
L:302 M:283 W: Missing Blank Line separator, <400> field identifier
L:302 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:302
L:308 M:283 W: Missing Blank Line separator, <220> field identifier
L:309 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>
ORGANISM:Artificial Sequence
L:309 M:283 W: Missing Blank Line separator, <400> field identifier
L:309 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:309

L:315 M:283 W: Missing Blank Line separator, <220> field identifier
L:316 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:16, <213>
ORGANISM:Artificial Sequence
L:316 M:283 W: Missing Blank Line separator, <400> field identifier
L:316 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:316
L:322 M:283 W: Missing Blank Line separator, <220> field identifier

VERIFICATION SUMMARY

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Input Set : A:\Sequence Listing for RECEPTOR FUNCTION REGULATING

AGENT.txt

Output Set: N:\CRF4\06082006\J580906.raw

L:323 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>
ORGANISM:Artificial Sequence

L:323 M:283 W: Missing Blank Line separator, <400> field identifier

L:323 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:323

L:329 M:283 W: Missing Blank Line separator, <220> field identifier

L:330 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:18, <213>
ORGANISM:Artificial Sequence

L:330 M:283 W: Missing Blank Line separator, <400> field identifier

L:330 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:18,Line#:330

L:336 M:283 W: Missing Blank Line separator, <220> field identifier

L:337 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:19, <213>
ORGANISM:Artificial Sequence

L:337 M:283 W: Missing Blank Line separator, <400> field identifier

L:337 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:337

L:343 M:283 W: Missing Blank Line separator, <220> field identifier

L:344 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:20, <213>
ORGANISM:Artificial Sequence

L:344 M:283 W: Missing Blank Line separator, <400> field identifier

L:344 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20,Line#:344